Claims

1. A method for identifying individuals susceptible to osteoarthritis comprising obtaining a sample of genomic DNA and detecting the presence or absence of any one of the 190 bp and the 200 bp allele of D2S325 from chromosome 2.

2. A method according to claim 1 for wherein the individuals are male.

3. A method for identifying individuals susceptible to osteoarthritis comprising obtaining a sample of genomic DNA and detecting the presence or absence of any one of the 192 bp, 202bp and 208 bp allele of D2S117 from chromosome 2.

4. A method according to claim 3 for identifying male individuals susceptible to osteoarthritis comprising obtaining a sample of genomic DNA and detecting the presence or absence of the 208 bp allele of D2S117 from chromosome 2.

5. A method according to claim 4 for identifying male individuals susceptible to osteoarthritis of the hip.

6. A method for isolating genetic loci associated with susceptability to OA comprising screening genomic libraries with sequence from the 190 bp allele of D2S325 and identifying open reading frames in regions adjacent to said allele.

7. A method for isolating genetic loci associated with susceptability to OA comprising screening a genomic library from an individual who is homozygote for the 190 bp allele of D2S325 and identifying open reading frames in regions adjacent to said allele.

8. A method for isolating genetic loci associated with susceptability to OA comprising identifying open reading frames in regions adjacent to D2S325 and comparing said open reading frames in individuals carrying a 190 bp allele of D2S325 with said open reading frames in individuals with a non-190 bp allele of D2S325.

9. A method for isolating genetic loci associated with susceptability to OA comprising screening genomic libraries with sequence from the 192 bp and 202 bp alleles of D2S117 and identifying open reading frames in regions adjacent to said allele.

10. A method for isolating genetic loci associated with susceptability to OA comprising screening a genomic library from an individual who is homozygote for any one of the 192 bp, the 202 bp and the 208 bp alleles of D2S117 and identifying open reading frames in regions adjacent to said allele.

11. A method for isolating genetic loci associated with susceptability to OA comprising identifying open reading frames in regions adjacent to D2S117 and comparing said open reading frames in individuals carrying any one of the 192 bp, 202bp and 208bp alleles of D2S117 with said open reading frames in individuals with other alleles of D2S117.

12. A method for isolating genetic loci according to any one of claims 7 to 11 in which open reading frames are identified within 500 Kb of said allele.

13. The use of the 190 bp allele of D2S325 as a marker for the identification of loci influencing susceptibility to OA.

14. The use of the 192 bp, 208bp and 202 bp alleles of

D2S117 as markers for the identification of loci influencing susceptibility to OA.

15. A method for mapping loci which affect susceptibility to OA by comparing genomic regions containing the 208 bp allele of D2S117 with genomic regions containing other alleles of D2S117.

16. A method for determining individual susceptibility to osteoarthritis comprising obtaining sample genomic DNA from siblings, at least two of which have clinical symptoms of osteoarthritis, analysing a region of their genomic DNA comprising a polymorphic marker, said region being located on chromosome 2q between D2S117 and D2S325, identifying allele sharing between the siblings as defined by a maximum log of the odds (LOD) score of greater than 1 and a p-value of less then 0.25, and determining individual susceptibility to osteoarthritis by reference to the allele sharing.

17. A method for determining individual susceptibility to osteoarthritis comprising obtaining sample genomic DNA from siblings, at least two of which have clinical symptoms of osteoarthritis, analysing a region of their genomic DNA comprising the polymorphic marker D2S114, identifying allele sharing between the siblings as defined by a maximum log of the odds (LOD) score of greater than 1 and a p-value of less then 0.25, and determining individual susceptibility to osteoarthritis by reference to the allele sharing.

18. A method for determining individual susceptibility to osteoarthritis comprising obtaining sample genomic DNA from siblings, at least two of which have clinical symptoms of osteoarthritis, analysing a region of their genomic DNA comprising a polymorphic marker, said region being located on chromosome 2q between D2S330 and D2S326, identifying allele

sharing between the siblings as defined by a maximum log of the odds (LOD) score of greater than 1 and a p-value of less then 0.25, and determining individual susceptibility to osteoarthritis by reference to the allele sharing.

19. A method for determining individual susceptibility to osteoarthritis according to any one of claims 13 to 15 in which one or more of the following genomic regions is additionally analysed; a genomic region comprising the polymorphic marker D6S273 and a genomic region comprising the polymorphic marker DXS1068.

20. A method for determining individual susceptibility to osteoarthritis comprising obtaining sample genomic DNA from siblings, at least two of which have clinical symptoms of osteoarthritis, analysing a region of their genomic DNA comprising any one of the polymorphic markers; D2S202, D3S1266, D4S231, D4S415, D6S260, D6S273, D6S286, D6S281, D7S669, D7S530, D11S907, D11S903, D11S901, D17S807, D17S789, DXS1068, identifying allele sharing between the siblings as defined by a maximum log of the odds (LOD) score of greater than 1 and a p-value of less then 0.25, and determining individual susceptibility to osteoarthritis by reference to the allele sharing.

21. A method for identifying loci conferring susceptibilty to osteoarthritis comprising screening a genomic library with genetic sequence derived from one or more of the following polymorphic markers; D2S202, D3S1266, D4S231, D4S415, D6S260, D6S273, D6S286, D6S281, D7S669, D7S530, D11S907, D11S903, D11S901, D17S807, D17S789, DXS1068 and identifying open reading frames in regions adjacent to the marker.

22. A method according to claim 18 in which the open reading frames identified are located within 500 Kb of the

polymorphic marker.